

R. Hutson



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/512,019

DATE: 12/20/2002

TIME: 11:07:58

Input Set : N:\Crf3\RULE60\09512019.raw

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1 <110> APPLICANT: HONG, GUOFAN
 2 HUANG, WEI-HUA
 3 <120> TITLE OF INVENTION: DNA POLYMERASE HAVING ABILITY TO REDUCE INNATE
 4 SELECTIVE DISCRIMINATION AGAINST FLUORESCENT
 5 DYE-LABELED DIDEOXYNUCLEOTIDES
 6 <130> FILE REFERENCE: hongsequencelisting
 7 <140> CURRENT APPLICATION NUMBER: 09/512,019
 8 <141> CURRENT FILING DATE: 2000-02-24
 10 <150> PRIOR APPLICATION NUMBER: US/09/157,397
 11 <151> PRIOR FILING DATE: 1998-09-21
 14 <150> PRIOR APPLICATION NUMBER: 08/544,643
 15 <151> PRIOR FILING DATE: 1995-10-18
 16 <150> PRIOR APPLICATION NUMBER: 08/642,684
 17 <151> PRIOR FILING DATE: 1996-05-03
 18 <160> NUMBER OF SEQ ID NOS: 11
 19 <170> SOFTWARE: PatentIn Ver. 2.0 - beta
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1764
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Bacillus stearothermophilus
 25 <400> SEQUENCE: 1
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 28 gccccgattg tcggaatcgc actagtgaac gagcatgggc gattttttat gcgcccggag 180
 29 accgcgctgg ctgattcgca attttttagca tggcttgccg atgaaacgaa gaaaaaaagc 240
 30 atgtttgacg ccaagcgggc agtcgttgcc ttaaagtga aaggaattga gcttcgcggc 300
 31 gtcgcctttg atttattgct cgctgcctat ttgctcaatc cggctcaaga tgccggcgat 360
 32 atcgctgcgg tggcgaaaat gaaacaatat gaagcgggtc ggtcgatga agcgggtctat 420
 33 ggcaaaggcg tcaagcggtc gctgccggac gaacagacgc ttgctgagca tctcgttcgc 480
 34 aaagcggcag ccatttgggc gcttgagcag ccgtttatgg acgatttgcg gaacaacgaa 540
 35 caagatcaat tattaacgaa gcttgagcac gcgctggcgg cgattttggc tgaaatggaa 600
 36 ttcaactggg tgaacgtgga taaaagcgg cttgaacaga tgggttcgga gtcgcccga 660
 37 caactgcgtg ccatcgagca gcgcatttac gagctagccg gccaaagagt caacattaac 720
 38 tcaccaaacc agctcggagt cattttatct gaaaagctgc agctaccggt gctgaagaag 780
 39 acgaaaacag gctattcgac ttcggctgat gtgcttgaga agcttgccgc gcatcatgaa 840
 40 atcgctgaaa acattttgca ttaccgccag cttggcaaac tgcaatcaac gtatattgaa 900
 41 ggattgttga aagttgtgcg ccctgatacc ggcaaagtgc atacgatgtt caaccaagcg 960
 42 ctgacgcaaa ctgggcggct cagctcggcc gagccgaact tgcaaaacat tccgattcgg 1020
 43 ctcgaagagg ggcggaataat ccgccaagcg ttcgtcccgt cagagccgga ctggctcatt 1080
 44 ttcgcccggc attactcaca aattgaattg cgcgctctcg cccatatcgc cgatgacgac 1140
 45 aatctaattg aagcgttcca acgcgatttg gatattcaca caaaaacggc gatggacatt 1200
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48 aaagaagctg ccgaatttat cgaacgttac ttcgccagct ttccggggcgt aaagcagtat 1380
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51 acggccatga acacgccaat tcaaggaagc gccgctgaca ttattaaaaa agcgatgatt 1560
52 gatttagcgg cacggctgaa agaagagcag cttcaggctc gtcttttgct gcaagtgcatt 1620
53 gacgagctca ttttggaaagc gccaaaagag gaaattgagc gattatgtga gcttggtccg 1680
54 gaagtgatgg agcaggccgt tacgctccgc gtgccgctga aagtcgacta ccattacggc 1740
55 ccaacatggt atgatgccaa ataa 1764
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58 <211> LENGTH: 587
59 <212> TYPE: PRT
60 <213> ORGANISM: Bacillus stearothermophilus
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63 1 5 10 15
64 Val Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
65 20 25 30
66 Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
67 35 40 45
68 Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu Ala
69 50 55 60
70 Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
71 65 70 75 80
72 Met Phe Asp Ala Lys Arg Ala Val Val Ala Leu Lys Trp Lys Gly Ile
73 85 90 95
74 Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Ala Ala Tyr Leu Leu
75 100 105 110
76 Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met Lys
77 115 120 125
78 Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Val
79 130 135 140
80 Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val Arg
81 145 150 155 160
82 Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp Leu
83 165 170 175
84 Arg Asn Asn Glu Gln Asp Gln Leu Leu Thr Lys Leu Glu His Ala Leu
85 180 185 190
86 Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp Thr
87 195 200 205
88 Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala
89 210 215 220
90 Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
91 225 230 235 240
92 Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
93 245 250 255
94 Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
95 260 265 270
96 Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
97 275 280 285

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100  Val Val Arg Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
101  305                               310                               315                               320
102  Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
103              325                               330                               335
104  Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
105              340                               345                               350
106  Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
107              355                               360                               365
108  Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
109              370                               375                               380
110  Ala Phe Gln Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
111  385                               390                               395                               400
112  Phe Gln Leu Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
113              405                               410                               415
114  Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
115              420                               425                               430
116  Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
117              435                               440                               445
118  Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
119              450                               455                               460
120  Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
121  465                               470                               475                               480
122  Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
123              485                               490                               495
124  Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
125              500                               505                               510
126  Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
127              515                               520                               525
128  Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
129              530                               535                               540
130  Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Glu Leu Val Pro
131  545                               550                               555                               560
132  Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
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134  Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
135              580                               585
137 <210> SEQ ID NO: 3
138 <211> LENGTH: 1764
139 <212> TYPE: DNA
140 <213> ORGANISM: Bacillus stearothermophilus
141 <400> SEQUENCE: 3
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144  gatgccccga ttgtcggaat cgactagtg aacgagcatg ggcgattttt tatgcgcccc 180
145  gagaccgcgc tggctgattc gcaattttta gcatggcttg cccgatgaaac gaagaaaaaa 240
146  agcatgtttg acgccaagcg ggcagtcgtt gccttaaagt ggaaaggaat tgagcttcgc 300
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148 gatatcgctg cgggtggcgaa aatgaaacaa tatgaagcgg tgcggtcgga tgaagcggtc 420
149 tatggcaaag gcgtcaagcg gtcgctgccg gacgaacaga cgcttgctga gcatctcggt 480
150 cgcaaagcgg cagccatttg ggcgcttgag cagccgttta tggacgattt gcggaacaac 540
151 gaacaagatc aattattaac gaagcttgag cacgcgctgg cggcgatttt ggctgaaatg 600
152 gaattcactg ggggtgaacgt ggatacaaaag cggcttgaac agatgggttc ggagctcgcc 660
153 gaacaactgc gtgccatcga gcagcgcatt tacgagctag ccggccaaga gttcaacatt 720
154 aactcaccaa aacagctcgg agtcatttta ttgaaaagc tgcagctacc ggtgctgaag 780
155 aagacgaaaa caggctattc gacttcggct gatgtgcttg agaagcttgc gccgcatcat 840
156 gaaatcgtcg aaaacatttt gcattaccgc cagcttggca aactgcaatc aacgtatatt 900
157 gaaggattgt tgaaagtgtg gcgcccgtgat accggcaaaag tgcatacgat gttcaaccaa 960
158 gcgctgacgc aaactgggcg gctcagctcg gccgagccga acttgcaaaa cattccgatt 1020
159 cggacccccac tggggcgga aatccgcaa gcgttcgtcc cgtcagagcc ggactggctc 1080
160 attttcgccg ccgattactc acaaattgaa ttgcgcgtcc tcgcccatac cgcgatgac 1140
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175 <212> TYPE: PRT

176 <213> ORGANISM: Bacillus stearothermophilus

177 <400> SEQUENCE: 4

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181 20 25 30
182 Glu Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala
183 35 40 45
184 Leu Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu
185 50 55 60
186 Ala Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys
187 65 70 75 80
188 Ser Met Phe Asp Ala Lys Arg Ala Val Val Ala Leu Lys Trp Lys Gly
189 85 90 95
190 Ile Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu
191 100 105 110
192 Leu Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met
193 115 120 125
194 Lys Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly
195 130 135 140
196 Val Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val
197 145 150 155 160

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204   Thr Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg
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206   Ala Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile
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210   Pro Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val
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212   Leu Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His
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215   290                               295                               300
216   Lys Val Val Arg Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln
217   305                               310                               315                               320
218   Ala Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln
219                               325                               330                               335
220   Asn Ile Pro Ile Arg Thr Pro Leu Gly Arg Lys Ile Arg Gln Ala Phe
221   340                               345                               350
222   Val Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln
223   355                               360                               365
224   Ile Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile
225   370                               375                               380
226   Glu Ala Phe Gln Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp
227   385                               390                               395                               400
228   Ile Phe Gln Leu Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln
229   405                               410                               415
230   Ala Lys Ala Val Asn Tyr Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly
231   420                               425                               430
232   Leu Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile
233   435                               440                               445
234   Glu Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn
235   450                               455                               460
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238   Arg Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg
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242   Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys
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244   Glu Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu
245   530                               535                               540
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